

FIGURE 1A

Input file Fbh56919FL2.seq  
Sequence length 3003

TTTCGGCACCAGCGCTGCTGCGGGGGGACTCTTTCTGAGGTTACTGTGGAGCACCCAAAGTCTGTCAGCCTCTGGCCGTGC  
AAACAGGCACCCAGAGGAACACAGACCTTGCTTATTACCCACAGCCTGGGACTGTCTTCTCCAGAGTCTCCATCAGCTT  
TGCTAATCGACTGATTGGAAATAATTCCTCAAAACACCACCAAGTCAAGGATACAGGCAGCAGCGGCTCCCTGTTGTGAT  
GGACATTCTGCACCCGAAACTGATAGCTGAGTCCCTGAAGTTTATGTTATGAAACAGAAGAAGTCTTATCCCTCAGCACAT  
M D E S A L T L G T I D V 13  
GATTTGGGAATTACACTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GGT ACA ATA GAT GTT 39  
S Y L P H S S E Y S V G R C K H T S E E 33  
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AAG CAC ACA AGT GAG GAA 99  
W G E C G F R P T V F R S A T L K W K E 53  
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA 159  
S L M S R K R P F V G R C C Y S C T P Q 73  
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TGT TAC TCC TGC ACT CCC CAG 219  
S W D K F F N P S I P S L G L R N V I Y 93  
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT 279  
I N E T H T R H R G W L A R R L S Y V L 113  
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT 339  
F I Q E R D V H K G M F A T N V T E N V 133  
TTT ATT CAA GAG CGA GAT GTG CAT AAG GGC ATG TTT GCC ACT GTG ACT GAA AAT GTG 399  
L N S S R V Q E A I A E V A A E L N P D 153  
CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT 459  
G S A Q Q Q S K A V N K V K K K A K R I 173  
GGT TCT GCC CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT 519  
L Q E M V A T V T S P A M I R A L T G W V L 193  
CTT CAA GAA ATG GTT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GGG TGG GTG CTG 579  
L K L F N S F F W N I Q I H K G Q L E M 213  
CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG 639  
V K A A T E T N L P L L F L P V H R S H 233  
GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT 699  
I D Y L L L T F I L F C H N I K A P Y I 253  
ATT GAC TAT CTG CTG CTC ACT TTC ATT CTC TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT 759  
A S G N N L N I P I F S T L I H K L G G 273  
GCT TCA GGC AAT AAT CTC AAC ATC TTA AGT ACC TTG ATC CAT AAG CTT GGG GGC 819  
F F I R R R L D E T P D G R K D V L Y R 293  
TTC TTC ATA CGA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA 879  
A T L H G H I V E L L R Q Q Q F L E I F 313  
GCT TTG CTC CAT GGT CAT AAT GTT GAA TTA CTT CGA CAG CAG CAA TTT TTG GAG ATC TTC 939  
L E G T R S R S G K T S C A R A G L L S 333  
CTG GAA GGC ACA CGT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA 999  
V V G V D T L S T N V I P D I L I I P V G 353  
GTT GTG GAT AAT CTG TCT ACC AAT GTC ATC CCA GAC ATC TTG ATA ATA CCT GTT GGA 1059

FIGURE 1B

I	S	Y	D	R	I	I	E	G	H	Y	N	G	E	Q	L	G	K	P	K	373	
ATC	TCC	TAT	GAT	CGC	ATT	ATC	GAA	GGT	CAC	TAC	AAT	GGT	GAA	CAA	CTG	GGC	AAA	CCT	AAG	1119	
K	N	E	S	L	W	S	V	A	R	G	V	I	R	M	L	R	K	N	Y	393	
AAG	AAT	GAG	AGC	CTG	TGG	AGT	GTA	GCA	AGA	GGT	GTT	ATT	AGA	ATG	TTA	CGA	AAA	AAC	TAT	1179	
G	C	V	R	V	D	F	A	Q	P	F	S	L	K	E	Y	L	E	S	Q	413	
GGT	TGT	GTC	CGA	GTG	GAT	TTT	GCA	CAG	CCA	TTT	TCC	TTA	AAG	GAA	TAT	TTA	GAA	AGC	CAA	1239	
S	Q	K	P	V	S	A	L	L	T	S	L	E	Q	A	L	L	P	A	I	433	
AGT	CAG	AAA	CCG	GTG	TCT	GCT	CTA	CTT	TCC	CTG	GAG	CAA	GGC	TTG	TTA	CCA	GCT	ATA	CTT	1299	
P	S	R	P	S	D	A	A	D	E	G	R	D	T	S	I	N	E	S	R	453	
CCT	TCA	AGA	CCC	AGT	GAT	GCT	GCT	GAT	GAA	GGT	AGA	GAC	ACG	TCC	ATT	AAT	GAG	TCC	AGA	1359	
N	A	T	D	E	S	L	R	R	R	L	I	A	N	L	A	E	H	I	L	473	
AAT	GCA	ACA	GAT	GAA	TCC	CTA	CGA	AGG	AGG	TTG	ATT	GCA	AAT	CTG	GCT	GAG	CAT	ATT	CTA	1419	
F	T	A	S	K	S	C	A	I	M	S	T	H	I	V	A	C	L	L	L	493	
TTT	ACT	GCT	AGC	AAG	TCC	TGT	GCC	ATT	ATG	TCC	ACA	CAC	ATT	GTG	GCT	TGC	CTG	CTC	CTC	1479	
Y	R	H	R	Q	G	I	D	L	S	T	L	V	E	D	F	F	V	M	K	513	
TAC	AGA	CAC	AGG	CAG	GGA	ATT	GAT	CTC	TCC	ACA	TTG	GTC	GAA	GAC	TTT	TTT	GTG	ATG	AAA	1539	
E	E	V	L	A	R	D	F	D	L	G	F	S	G	N	S	E	D	V	V	533	
GAG	GAA	GTC	CTG	GCT	CGT	GAT	TTT	GAC	CTG	GGG	TTT	TCA	GGA	AAT	TCA	GAA	GAT	GTA	GTA	1599	
M	H	A	I	Q	L	L	G	N	C	V	T	I	T	H	T	S	R	N	D	553	
ATG	GAT	GCC	ATA	CAG	CTG	CTG	GGA	AAT	TGT	GTC	ACA	ATC	ACC	CAC	ACT	AGC	AGG	AAC	GAT	1659	
E	F	F	I	T	P	S	T	T	V	P	S	V	F	E	L	N	F	Y	S	573	
GAG	TTT	TTT	ATC	ACC	CCC	AGC	ACA	ACT	GTC	CCA	TCA	GTC	TTT	GAA	CTC	AAC	TTC	TAC	AGC	1719	
N	G	V	L	H	V	F	I	M	E	A	I	I	A	C	S	L	Y	A	V	593	
AAT	GGG	GTA	CTT	CAT	GTC	TTT	ATC	ATG	GAG	GCC	ATC	ATA	GCT	TGC	AGC	CTT	TAT	GCA	GTT	1779	
L	N	K	R	G	L	G	G	P	T	S	T	P	P	N	L	I	S	Q	E	613	
CTG	AAC	AAG	AGG	GGA	CTG	GGG	GGT	CCC	ACT	AGC	ACC	CCA	CCT	AAC	CTG	ATC	AGC	CAG	GAG	1839	
Q	L	V	R	K	A	A	S	L	C	Y	L	L	S	N	E	G	T	I	S	633	
CAG	CTG	GTG	CGG	AAG	GCG	GCC	AGC	CTG	TGC	TAC	CTT	CTC	TCC	AAT	GAA	GGC	ACC	ATC	TCA	1899	
L	P	C	Q	T	F	Y	Q	V	C	H	E	T	V	G	K	F	I	Q	Y	653	
CTG	CCT	TGC	CAG	ACA	TTT	TAC	CAA	GTC	TGC	CAT	GAA	ACA	GTA	GGA	AAG	TTT	ATC	CAG	TAT	1959	
G	I	L	T	A	E	H	D	D	Q	E	D	I	A	S	P	S	L	A	E	673	
GGC	ATT	CTT	GTA	GTG	GCA	GAG	CAC	GAT	GAC	Q	E	GAT	ATC	AGT	CCT	AGT	CTT	GCT	GAG	2019	
Q	Q	W	D	K	K	L	P	E	P	L	S	W	R	S	D	E	E	D	E	693	
CAG	CAG	TGG	GAC	AAG	AAG	CTT	CCA	GAA	CCT	TTG	TCT	TGG	AGA	AGT	GAT	GAA	GAA	GAT	GAA	2079	
D	S	D	F	G	E	E	Q	R	D	C	Y	L	K	V	S	Q	S	K	E	713	
GAC	AGT	GAC	TTT	GGG	GAG	GAA	CAG	GGA	GAT	TGC	TAC	CTG	AAG	GTG	AGC	CAA	TCC	AAG	GAG	2139	
H	Q	Q	F	I	T	F	L	Q	R	A	L	L	G	P	L	L	E	A	Y	733	
CAC	CAG	CAG	TTT	ATC	ACC	TTC	TTA	CAG	AGA	CTC	CTT	GGG	CCT	TTG	CTG	GAG	GCC	TAC	AGC	2199	
S	A	A	I	F	V	H	N	F	S	G	P	V	P	E	P	E	Y	L	Q	753	
TCT	GCT	GCC	ATC	TTT	GTT	CAC	AAC	TTC	AGT	GGT	CCT	GTT	CCA	GAA	CCT	GAG	TAT	CTG	CAA	2259	
K	L	H	K	K	Y	L	I	T	R	T	E	R	N	V	A	V	Y	A	E	S	773
AAG	TTG	CAC	AAA	TAC	CTA	ATA	ACC	AGA	ACA	GAA	AGA	AAT	GTT	GCA	GTA	TAT	GCT	GAG	AGT	2319	

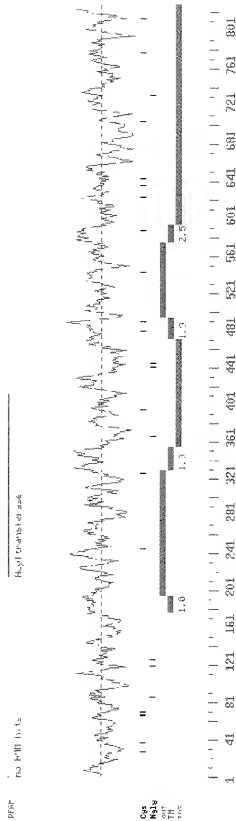
FIGURE 1C

A	T	Y	C	L	V	K	N	A	V	K	M	F	K	D	I	G	V	F	K		793
GCC	ACA	TAT	TGT	CTT	GTG	AAG	AAT	GCT	GTG	AAA	ATG	TTT	AAG	GAT	ATT	GGG	GTT	TTC	AAG		2379
E	T	K	Q	K	R	V	S	V	L	E	L	S	S	T	F	L	P	Q	C		813
GAG	ACC	AAA	CAA	AAG	AGA	GTG	TCT	GTT	TTA	GAA	CTG	AGC	AGC	ACT	TTT	CTA	CCT	CAA	TGC		2439
N	R	Q	K	L	L	E	Y	I	L	S	F	V	V	L	*						829
AAC	CGA	CAA	AAA	CTT	CTA	GAA	TAT	ATT	CTG	AGT	TTT	GTG	GTG	CTG	TAG						2487

GTAACGTGTGGCACTGCTGGCAAATGAAGGTCATGAGATGAGTTCCTTGTTAGGTACCAGCTTCTGGCTCAAGAGTTTGA  
 AGGTGCCCTTCGCAGGGGTCAGGCCCTGCCCTGTNCCGAAGTGATCTCCTGGAAGACAAGTGCCTTCTNCTCCATGGATC  
 TGAGATCTTCCCAGCTTT

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Figure 2



>56919  
 MDESNLTGLTIDVSLPHSESVGRCKHSEWGECPRTVFRSNTLKKWSLSMSRR  
 PVORCCSCTPQSDKDFNFSIPISGLRNVIYINETHIRGMLARLSYLFQERDV  
 HGFMTNTENVLMSKRVQEAIAEVAELNPDGSAQQSKAVNKKKAKRLLQEWAT  
 VSFAMRLTGMWLLKFNFTFMIQIHGQLEWYAAETNPLLPVPHSHDYLILT  
 FLFCHNIKAFYIAGNNNTIPFSTLIHKLGGFFIRRLDETPOGRKDVLYRALHGH  
 VELLRQQQFTEIFLEGTGRSGKTSKAGLISVVVDLTSTNVPDILIPYGISYDRII  
 EGHYNQELGPKPKMSLMSVARGVIRMKRNKVCYVDFAQFPFSKEYLESQKPFVA  
 LLSLEQALLPAILPERSDAADGRDTSINERNATDESIRRLIANLAHHTILPTASKC  
 ATWSTHIVACULLVEHQIGDILTLVDEPTWKEFVLARDPGLQPSGSDVWMAIQL  
 GNCVTIHSRNDPEPTPSITVPSVFLNFTSYNGVLHVFIMEALTACSLVANLKHGLG  
 GTSTPMLISQBQVAKZAGLCILLNBSGISLPCQTFVQCHETVOKFIQIGLTVAE  
 HDDQEDISPAIDQWOKKLEFLNMSDEDESDPGEQRDCTLKVSQSKEHQQITP  
 LQRLGLPGLERAYSSAALFVHNSGVPPEYIQLKHLKYLITERNVAVASATYCLVK  
 NAVMFKFDIGVFRETQKRVSVLELSSTFLPQCNRQKLEYLTSFVVL

Figure 3

## Protein Family / Domain Matches, HMMer version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMer 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMer is freely distributed under the GNU General Public License (GPL).
-----
HMM file:                /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
Sequence file:           /prod/ddm/wspace/orfanal/oa-script.21255.seq
-----
Query: 56919
```

```
Scores for sequence family classification (score includes all domains):
Model      Description                Score    E-value    N
-----
Acyltransferase  Acyltransferase                126.1     6.4e-34
1
```

```
Parsed for domains:
Model      Domain  seq-f  seq-t    hmm-f  hmm-t    score    E-value
-----
Acyltransferase  1/1      215    412 ..      1    195 []    126.1    6.4e-34
```

Alignments of top-scoring domains:

```
Acyltransferase: domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34
*->lenlpkkgpaivvsNhrSylDilvlsaalprrgpwlvrirvfiakke
+ +++++ p ++ + HrS++D+l+l ++l++++ ++ +ia ++
56919 215 KAAATETNLPFLFLPVHRSHIDYLLLTFLFCHN---IKAPYIASGN 257

llkvPlIfGwmlrлагаifidRnnra....kdalaaadelvrvlellrk
+l++P+ f++l+ ++g +fi+R+ ++++++kd l++a+ + +ellr+
56919 258 NLNIPI-FSTLIHKLGFFIRRLDEtpdgrKDVLRYALLGHGHIIVELLRQ 306

grsvliFPEGTRsrsgellppfKkGia....afrlAlkagvpivPvviv
+ + iF EGTRsrsg++ + ++G+++ + + ++ ++ i+PV+i
56919 307 QQFLIEFLGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILIIIPVGI- 354

sgteelepknagkllrlarkkgpvtvrvlppipld..pedikelaerlr
s++ ++e ++++ + ++kk++++ V +++ ++++ +++++ +
56919 355 SYDRIIEGHYNGEQ--LGKPKKNESLWSVARGVIRM1rKNYGCVRVDFQA 402

diltvgaleel<-*
+ +++++ e+
56919 403 PPSLKYLESL 412
```

Figure 4A

ProDom Matches					Score
ProdomId	Start	End	Description		
View Prodom PD347660	1	55	p2001.1 (2) PLSB (2) // ACYLTRANSFERASE	250	
			PHOSPHOLIPID BIOSYNTHESIS PRECURSOR		
			TRANSMERANE GLYCEROL-3-PHOSPHATE		
			GPAT MITOCHONDRION MITOCHONDRIAL		
View Prodom PD087501	51	158	p2001.1 (1) // AIP2-DLD1	77	
View Prodom PD353751	56	152	p2001.1 (2) PLSB (2) // ACYLTRANSFERASE	500	
			PHOSPHOLIPID BIOSYNTHESIS PRECURSOR		
			TRANSMERANE GLYCEROL-3-PHOSPHATE		
			GPAT MITOCHONDRION MITOCHONDRIAL		
View Prodom PD037846	128	259	p2001.1 (15) PLSB (5) DAPT (2) //	258	
			ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE		
			PHOSPHOLIPID GPAT BIOSYNTHESIS		
			MITOCHONDRIAL TRANSMERANE		
View Prodom PD042466	259	590	PRECURSOR MITOCHONDRION	413	
			p2001.1 (16) PLSB (4) DAPT (2) //		
			ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE		
			BIOSYNTHESIS PHOSPHOLIPID GPAT		
View Prodom PD025192	462	649	PRECURSOR MITOCHONDRIAL	458	
			TRANSMERANE MITOCHONDRION		
			p2001.1 (4) PLSB (3) // ACYLTRANSFERASE		
			PHOSPHOLIPID MITOCHONDRIAL		
View Prodom PD042027	465	673	BIOSYNTHESIS PRECURSOR TRANSMERANE	80	
			GLYCEROL-3-PHOSPHATE GPAT		
			MITOCHONDRION		
			p2001.1 (6) PLSB (2) // ACYLTRANSFERASE		
View Prodom PD042760	650	828	GLYCEROL-3-PHOSPHATE MEMBRANE	799	
			PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT		
			p2001.1 (2) PLSB (2) // ACYLTRANSFERASE		
			PHOSPHOLIPID BIOSYNTHESIS PRECURSOR		
			TRANSMERANE GLYCEROL-3-PHOSPHATE		
			GPAT MITOCHONDRION MITOCHONDRIAL		

Figure 4B

View Prodom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS  
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION  
 MITOCHONDRIAL  
 Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79  
 Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FTQYGILTVAEHDQEDISPSLAEQWDKLPPELSNRXXXXXXXXXXXXXQRCYLYKS 709  
 FTQYGILTVAB DPED+SP LAQQW+KLPPEL+NR QRCYLYKS  
 Sbjct: 1 FTQYGILTVAEQDQEDVSPGLAEQWKKLPPELNRSDEDESDPGEQRCYLYKS 60

Query: 710 QSKHQQFTTFQRLGLPILAEYSSAIFVNFSGPVPPEYQKLHKYLIITRERNVAV 769  
 Q+KSHQQFTTFQRLGLPILAEYSSAIFVNF GPVPE EYQKLH+YLIITRERNVAV  
 Sbjct: 61 QAKHQQFTTFQRLGLPILAEYSSAIFVNFSGPVPPEYQKLHKYLIITRERNVAV 120

Query: 770 YAESATYCLVKNVAMFKDIGFKETQRVSVELSSTFLPQCNQKLLLEYILSFVWL 828  
 YAESATYCLVKNVAMFKDIGFKETQKR SVLELS+TFPLPQCNQKLLLEYILSFVWL  
 Sbjct: 121 YAESATYCLVKNVAMFKDIGFKETQKRASVLELSSTFLPQCNQKLLLEYILSFVWL 179

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS  
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION  
 MITOCHONDRIAL  
 Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47  
 Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSKRKPFVGRCCVCTPQSNKDFNPSPISGLGRNVIYNETHTRHGNLARRLSYVLFI 115  
 MSKRKPFVGRCCVCTPQSN++FPSPISGLGRNVIYNETHTRHGNLARRLSY+LF+  
 Sbjct: 1 MSKRKPFVGRCCVCTPQSWRFNPSPISGLGRNVIYNETHTRHGNLARRLSYILFV 60

Query: 116 QERDVHKGWFATNTVENSRRVQEAIAEVAELNP 152  
 QERDVHKGWFAT++T+NVLSNRRVQEAIAEVAELNP  
 Sbjct: 61 QERDVHKGWFATSTIDNVLSNRRVQEAIAEVAELNP 97

Figure 4C

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View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL
BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT
MITOCHONDRION
Length = 194

Score = 450 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43
Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RELIANLAELHILFTASKCAINSTHIVACLLLYRRHQIDLSTLVDFVFMKEVLARDF 521
      R LI ++ EH++P S C+INSTH+VACLLL R G+ STL ED + E++LA
Sbjct: 3 RNLIRGIEHVHVPDCSNMCSINSTHIVACLLATWRNGVHRSTLEEDCDMLCEKILAEQ 62

Query: 522 DL-GPGSNS--EDVWHAIGLLGNCVTTHTSRDEFFITPTTVPSPFLNFSNGVL 577
      D+ GFGS S ++V +A ILLG+CVT+T RNDPE+L+P +VPS EL +YSN V+
Sbjct: 63 DIVGFGKSTGSGQVYKACELGSGCTVIDERNDDEFYISPKNSVPSFIELAYNSVI 122

Query: 578 HVFIMEAIIACSLYAVLNKRGLOGFTPTPNLISQELVVRKASLCVLLSNEGTSISLPQ 637
      F +++IIAC++Y++ NK G3 NLISSQELV A SLC L E PQ
Sbjct: 123 CHFALKSIITACTIYSLPNKTKNGEGAGLNLISQELVEDALSICDMLQYEFMFCRFPQ 182

Query: 638 TFYQVCHETVGK 649
      T ++CH T+GK
Sbjct: 183 TLRELCHNTLQK 194

```



Figure 4D

View Prodom PD042466

>PD042466 p2001.1 (16) PLB (4) DAPT (2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE  
BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE  
MITOCHONDRION  
Length = 299

Score = 413 (150.4 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42  
Identities = 79/152 (51%), Positives = 108/152 (71%)

Query: 259 LNIPIFSLIHLKGGFFIRRLDETPDGKRDVLYRALLHGHIVELLRQOQLEIFLESTR 318

L+PI +L+ + G FPIR D TP-G+ D LYR+ H ++ +L+ + +E F+EGTR

Subject: 2 LSNPIGSLIRRTGAFFIRSDPTPGKQDLYRAVFHYVAGLISKGYNIEFFIEGTR 61

Query: 319 SRSGTSCARAGLSVVDTLSTNVIPDLIIPWGISVDRIEGH-INGEOLGPKKNES 377

SP+GK +GLS+VVA+ +PDIL+PV ISVDRIEG+ Y E G PKK ES

Subject: 62 STGKMLPKTKGLSNVVEATLGSVPDILLVPVLSISYDRILEGNTYHIELRGAPKKES 121

Query: 378 LMSVARGVIRMLRNNGYGVVDPAQPSLKEY 409

LW + RGV +ML+-NYG V VDF +P SL+EY

Subject: 122 LQQLFRGVKRLKNGYGVYVDRGPISLREY 153

Score = 64 (27.6 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42  
Identities = 30/143 (20%), Positives = 59/143 (41%)

Query: 453 RNATDESRLRLIANLAELILFTASKSCAINSHIVACILLNHRHOGIDISTL---VEDP 509

RN + +R + ++ + ++ + +T +V+ LL+ + L L +4D

Subject: 160 RTYNCAFKRLAQKMSFEVAMRILOATPTATGIVSALLITRGALTLDQLHHTLAQS 219

Query: 510 FOMKEVLARDFDLQFSNDSVDVHAIQLL--GRCVTIHTSRNDEFFITSTVPSVF 567

E + S + V A L G+ VT + R +I+ P + P

Subject: 220 LDYLERKQSPVTSALRLRSRGVRAADALSNGHVTVDGSEPPWYIAPDDEHAAP 279

Query: 568 ELNPFYNGVLIHVFINEALLACSL 590

Y N V+H P+ +I+ +L

Subject: 280 ----YRNSVHAFLTSIVELAL 298

Figure 4E

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View Prodom PD037846
>PD037846 p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR
MITOCHONDRIAL
Length = 345

Score = 258 (95.9 bits), Expect = 3.4e-21, P = 3.4e-21
Identities = 56/132 (42%), Positives = 79/132 (59%)

Query: 128 NVTNVLNSRQVQEAIAEVAELNPDGSAQQSQXXXXXXXXXXARLQORVATVSPAMIR 187
      N+ -NVINS + I + A++ S IL EM T++ MIR
Sbjct: 223 NLKKNVLSSEIHVIEQ-----EAKSSSTIDKVRREAREILDMSHTLNMGIR 273

Query: 188 LTGWLLKLNFSFNNIQTWKQLEWKAATELNPLFLPVHRSHIDYLLLTFLFCHN 247
      GWVL K+FN F I+++ Q+E +K ATE P++LP HRSHIDYLL+FIL+ ++
Sbjct: 274 FCGVLKSKTFNRIFSGICVNEEQIEKIKGATEQGHVILPVRSHIDYLLSLFLHYD 333

Query: 248 IKAPYIASGNL 259
      IK P+IA+G NL
Sbjct: 334 IKVPHIAGNLL 345

View Prodom PD347660
>PD347660 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRIAL
MITOCHONDRIAL
Length = 55

Score = 250 (93.1 bits), Expect = 2.4e-20, P = 2.4e-20
Identities = 43/55 (78%), Positives = 53/55 (96%)

Query: 1 MDESALTGLTIDVSLPHSSEYSVGRCHTSEWGEQGFPTVFSATLKWKESL 55
      M+ES++T+GTIDVSLP+SSSEYS+GRCHT+E+W -CGF+PT FRSATLKWKESL
Sbjct: 1 MEESVTIGTIDVSLPNSSEYSIGRCHTNEDWDGCFKPTFFFSATLKWKESL 55

```

Figure 4f

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View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE
    PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT
    Length = 345

    Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10
    Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAELHIFTASKSCAIMSTHIVACLLYHRQIDSLTIVE--DFPWKEEVIARDFD 522
      +LA+ I+ + + A+ ++ A LL ++ + LAE D ++ + D
Sbjct: 32 VNHLLAQIMTHINDAAVNPMLCATALLSTQRALGEGQLIEQDCYLKLRNVFYSTD 91

Query: 523 LGFSGRS-EDVVMHAIQ--LIGNCVTITHSRNDEFFFTPTSTVPSEFNFNFYNGVLHV 579
      + + E + HA Q LIG VT+ + D + V + + Y N VLH+
Sbjct: 92 ATLDPHTERLEIHAHQMLLG--VTVEKOTLGDILRLDSNAVL---MTYRNVLHL 145

Query: 580 FMEAILIAC 588
      F + A++AC
Sbjct: 146 FALPALVAC 154

    Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10
    Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 LNFYSNGVLHVFMEALIALCSLYLVNKGGLGFTSTFNPILISQFOLYKASLCYLLSN 628
      + Y N VLH+F + A++AC N+R IS++ L+R +L L
Sbjct: 135 MTYRNVLHLFALPALVACCFKN-NRR-----ISRDLALRFVFAIIPFLQA 180

Query: 629 EGTISLPQCTFYGVCHETVGKFIQYIGILTVAEHDQEDISPSLAE 673
      E + + + +F++ G+L A + + ++ + ++
Sbjct: 181 ELFLRWNEDELNDHIDQWINEFVRQGLLSAGNQEDDLTRNTSQ 225

```

TOTERO\*00256000

Figure 4G

```
View Prodom PD087501
>PD087501.p2001.1 (1) // AIP2-DLD1
Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994
Identities = 31/114 (27%), Positives = 44/114 (38%)

Query: 51 WTES--LMSRRPFVGRCCYCTPQSDWDFNPSIPSLGLRNVIYINETHTRKGLARR 108
      W ES L+ RK F RCC P K + L N +H W
Sbjct: 12 WNESEVLVDRKSKFQARCC---PLQKQDIPSIQLQELTQNNKSVSKASHMNYAMRTAE 67

Query: 109 LSYVLFQIERDYHKGMAFNVTENVLNSSR--VQ-EAIAEYAAELNPDGSAQQ 158
      +S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+
Sbjct: 68 VNNHLQQEQKKKGKNNKNNSHWKSBNITVQPKNIQGCDCGEGAGQR 121
```

FIGURE 5A

	10	20	30	40	
1	MDESALT	LGTDVSYLP	HSSEYSVGRCK	HTSEEWGECG	F56919.pro
1	MEESSVT	VGTDVSYLP	SSSEYSLGRCK	HTSEDWVDCG	F56919.pro
1	MEESSVT	IGTDVSYLP	NSSEYSLGRCK	HTNEDWVDCG	F56919.pro
	50	60	70	80	
41	PTVFRSAT	LKWKESLMSR	KRPFVGRCCY	SCTPQSWDKFF	N56919.pro
41	PTFFRSAT	LKWKESLMSR	KRPFVGRCCY	SCTPQSWERFF	N56919.pro
41	PTFFRSAT	LKWKESLMSR	KRPFVGRCCY	SCTPQSWERFF	N56919.pro
	90	100	110	120	
81	PSIPSLGL	RNVIIYINETH	TRHRGWLARR	LSYVLFIQERD	V56919.pro
81	PSIPSLGL	RNVIIYINETH	TRHRGWLARR	LSYILFVQERD	V56919.pro
81	PSIPSLGL	RNVIIYINETH	TRHRGWLARR	LSYILFVQERD	V56919.pro
	130	140	150	160	
121	HKGMFATN	VTVENVLN	SSSRVQEATA	EVAAELNPDG	SAQQQS56919.pro
121	HKGMFATN	VTVENVLN	SSSRVQEATA	EVAAELNPDG	SAQQQS56919.pro
121	HKGMFATN	VTVENVLN	SSSRVQEATA	EVAAELNPDG	SAQQQS56919.pro
	170	180	190	200	
161	KAVNVKVK	KKAKRILQ	EMVATVSPAM	IRLTGWVLLK	LFNSSF56919.pro
161	KAVNVKVK	KKAKRILQ	EMVATVSPAM	IRLTGWVLLK	LFNSSF56919.pro
161	KAVNVKVK	KKAKRILQ	EMVATVSPAM	IRLTGWVLLK	LFNSSF56919.pro
	210	220	230	240	
201	FWNIQIHK	GQLEMVKA	AATETNLP	LFLFLPVHR	SHIDYLLLT56919.pro
201	FWNIQIHK	GQLEMVKA	AATETNLP	LFLFLPVHR	SHIDYLLLT56919.pro
201	FWNIQIHK	GQLEMVKA	AATETNLP	LFLFLPVHR	SHIDYLLLT56919.pro
	250	260	270	280	
241	FILFCHNIK	APYIASGN	NLNIPFSTLI	HKLGGF	FIRRRRL56919.pro
241	FILFCHNIK	APYIASGN	NLNIPFSTLI	HKLGGF	FIRRRRL56919.pro
241	FILFCHNIK	APYIASGN	NLNIPFSTLI	HKLGGF	FIRRRRL56919.pro
	290	300	310	320	
281	DETPDGRK	DVLYRALL	HGHIVELL	RQQQFLEIF	LEGTRSR56919.pro
281	DETPDGRK	DVLYRALL	HGHIVELL	RQQQFLEIF	LEGTRSR56919.pro
281	DETPDGRK	DVLYRALL	HGHIVELL	RQQQFLEIF	LEGTRSR56919.pro
	330	340	350	360	
321	SGKTSCAR	AGLLSVV	VDTLSTNV	IPDILIPVG	ISYDRII56919.pro
321	SGKTSCAR	AGLLSVV	VDTLSTNV	IPDILIPVG	ISYDRII56919.pro
321	SGKTSCAR	AGLLSVV	VDTLSTNV	IPDILIPVG	ISYDRII56919.pro

FIGURE 5B

	370	380	390	400	
361	EGHYNGEQLGKPKKKNESLWSVARGVIRMLRKNYGCVRVDF				56919.pro
361	EGHYNGEQLGKPKKKNESLWSVARGVIRMLRKNYGYVRVDF				MouseGPAT.PRO
361	EGHYNGEQLGKPKKKNESLWSVARGVIRMLRKNYGYVRVDF				RatGPAT.PRO
	410	420	430	440	
401	AQPFSLKEYLESQSQKPVSAALLSLEQALLPAILPSRPSDA				56919.pro
401	AQPFSLKEYLEGGQSQKPVSAPLSLEQALLPAILPSRPNDV				MouseGPAT.PRO
401	AQPFSLKEYLEGGQSQKPVSAPLSLEQALLPAILPSRPDA				RatGPAT.PRO
	450	460	470	480	
441	ADEGRDTSINESRNATDES LRRRLIANLAEHILFTASKSC				56919.pro
441	ADEHQDLSNESRNPADEAFRRRLIANLAEHILFTASKSC				MouseGPAT.PRO
441	AAEHEDMSSNESRNAADEAFRRRLIANLAEHILFTASKSC				RatGPAT.PRO
	490	500	510	520	
481	AEMSTHIVACLLLYRHRQGIDLSTLVEDFFVMKEEVLARD				56919.pro
481	AEMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD				MouseGPAT.PRO
481	AEMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD				RatGPAT.PRO
	530	540	550	560	
521	FDLGFGSGNSEDVVMHAIQLLGNCVTITHTSRNDEFFFITPS				56919.pro
521	FDLGFGSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFFITPS				MouseGPAT.PRO
521	FDLGFGSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFFITPS				RatGPAT.PRO
	570	580	590	600	
561	TTVPVSVFELNIFYSNGVLHV FIMEAIIACSLYAVLNKRGLG				56919.pro
561	TTVPVSVFELNIFYSNGVLHV FIMEAIIACSIYAVLNKRCSG				MouseGPAT.PRO
561	TTVPVSVFELNIFYSNGVLHV FIMEAIIACSIYAVQNKRGSG				RatGPAT.PRO
	610	620	630	640	
601	GPTSTTPPNLISQEQLVKKAASLCYLLSNEGTTISLPCQTFY				56919.pro
601	GSAGGLGNLISQEQLVKKAASLCYLLSNEGTTISLPCQTFY				MouseGPAT.PRO
601	GSAGGLGNLISQEQLVKKAASLCYLLSNEGTTISLPCQTFY				RatGPAT.PRO
	650	660	670	680	
641	QVCHETVGKFIQYQILTVAEHDDQEDISP SLAEQQWDDKKL				56919.pro
641	QVCHETVGKFIQYQILTVAEQDDQEDVSPGLAEQQWDDKKL				MouseGPAT.PRO
641	QVCQETVGKFIQYQILTVAEQDDQEDVSPGLAEQQWNNKKL				RatGPAT.PRO
	690	700	710	720	
681	PEPLSWRSDEEDEDSDFGEEQRDCYLKVSQSKEHQQFITF				56919.pro
681	PE-LNWRSD E EDEDSDFGEEQRDCYLKVSQSKEHQQFITF				MouseGPAT.PRO
681	PEPLNWRSD E EDEDSDFGEEQRDCYLKVSQAKEHQQFITF				RatGPAT.PRO

FIGURE 5C

	730	740	750	760		
721	LQRL	LGPL	LEAYSSAAIFVHN	FSGPVP	EEPEY LQKLHKYLI	56919.pro
720	LQRL	LGPL	LEAYSSAAIFVHN	FSGPVP	EESEY LQKLHRYLI	MouseGPAT.PRO
721	LQRL	LGPL	LEAYSSAAIFVHT	FRG	PVPESEY LQKLHRYLL	RatGPAT.PRO
	770	780	790	800		
761	TRTER	NVAVY	AESATYCLVKN	AVKMFKD	IGVFKETKQKRV	56919.pro
760	TRTER	NVAVY	AESATYCLVKN	AVKMFKD	IGVFKETKQKRV	MouseGPAT.PRO
761	TRTER	NVAVY	AESATYCLVKN	AVKMFKD	IGVFKETKQKRA	RatGPAT.PRO
	810	820				
801	SVLE	LSST	FLPQCN	RQKL	LEYILSFVVL	56919.pro
800	SVLE	LSST	FLPQCN	RQKL	LEYILSFVVL	MouseGPAT.PRO
801	SVLE	LSST	FLPQGS	RQKL	LEYILSFVVL	RatGPAT.PRO

721  
 720  
 721  
 761  
 760  
 761  
 801  
 800  
 801

# Acyltransferase catalytic motif-I

I F L E G T R S R	56919.pro
I F L E G T R S R	MouseGPAT.PRO
I F L E G T R S R	RatGPAT.PRO
Y F V E G G R S R	EcoliGPAT.PRO

# Acyltransferase catalytic motif-II

H R S H I D	56919.pro
H R S H I D	MouseGPAT.PRO
H R S H I D	RatGPAT.PRO
H R S H M D	EcoliGPAT.PRO

# Acyltransferase catalytic motif-III

I L I I P V	56919.pro
I L V I P V	MouseGPAT.PRO
I L V I P V	RatGPAT.PRO
I T L I P I	EcoliGPAT.PRO

# Acyltransferase signature motif

G G F F I R R	56919.pro
G G F F I R R	MouseGPAT.PRO
G G F F I R R	RatGPAT.PRO
G A F F I R R	EcoliGPAT.PRO

**FIGURE 6**





FIGURE 8

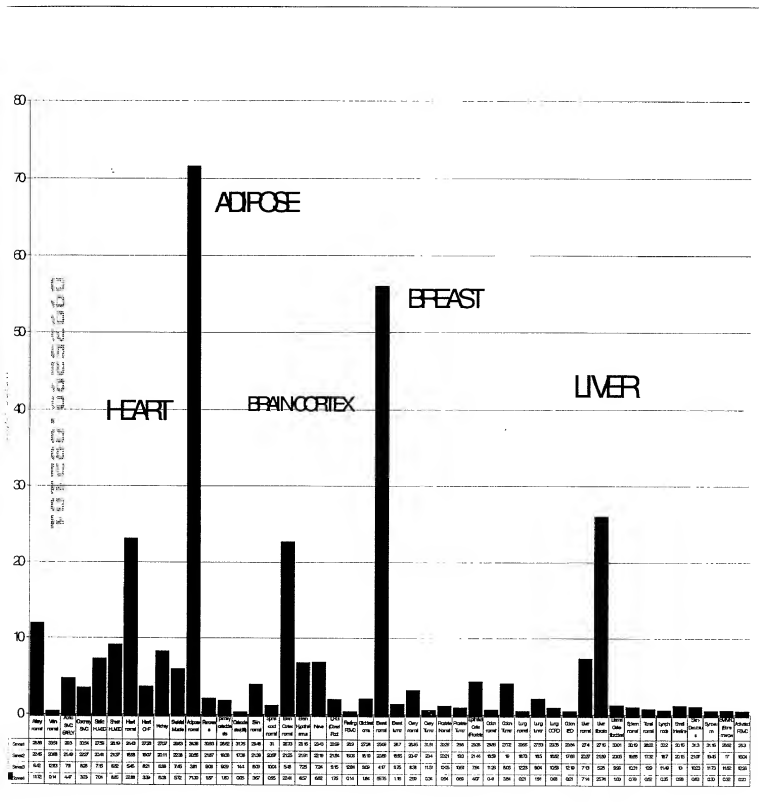


FIGURE 9

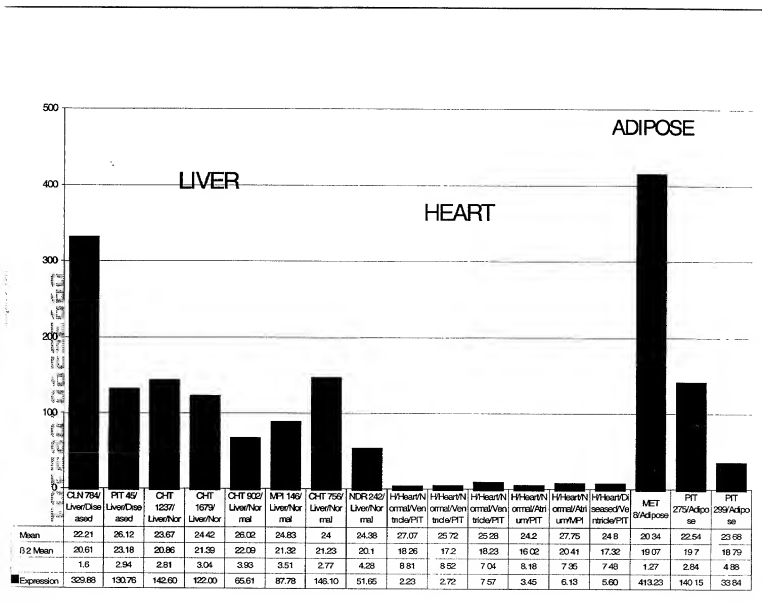


FIGURE 10A

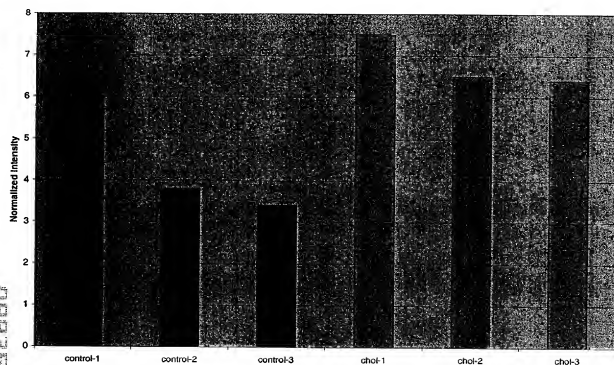


FIGURE 10B

